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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 2772.05 Seconds  
(without alignments)  
11181.073 Million cell updates/sec

Title: US-09-922-895-2

Perfect score: 1065

Sequence: 1 ATGACACCTCCTAGATAC.....CGGAACCTCTATTGCTTT 1065

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb\_ba:\*  
2: gb\_htg:\*  
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17: em\_hum:\*  
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19: em\_mu:\*  
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30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
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36: em\_htg\_mam:\*  
37: em\_htg\_vtl:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	100.0	1065	6 AR164119	AR164119 Sequence
2	1065	100.0	1065	6 AX030929	AX030929 Sequence
3	1065	100.0	1068	9 AF026535	AF026535 Homo sapi
4	1065	100.0	1201	9 HSU28654	HSU28654 Human eosin
5	1065	100.0	1717	6 AX334894	AX334894 Sequence
6	1065	100.0	1717	6 HSU51241	HSU51241 Human eosin
7	1065	100.0	1915	6 BD06761	BD06761 Chemokine
8	1065	100.0	5791	9 AF247361	AF247361 Homo sapi
9	1065	100.0	197279	9 AC104439	AC104439 Homo sapi
10	1065	100.0	220865	2 HSA312688	HSA312688 Homo sapi
11	1061.8	99.7	1068	6 AX280851	AX280851 Sequence
12	1061.8	99.7	1689	6 AX323054	AX323054 Sequence
13	1061.8	99.7	1689	6 HSU49727	HSU49727 Human C-C
14	1060.2	99.5	1068	9 AB023887	AB023887 Homo sapi
15	980.2	92.0	1068	9 CAY13775	CAY13775 Cercopithe
16	977	91.7	1068	9 AY065647	AY065647 Macaca fa
17	975.4	91.6	1068	9 AY065646	AY065646 Macaca fa
18	975.4	91.6	1068	9 MMY13776	MMY13776 Macaca mu
19	975.4	91.6	1108	9 AF291668	AF291668 Macaca fa
20	972.2	91.3	1068	9 AF017283	AF017283 Macaca mu
21	713	66.9	7201	6 AX345239	AX345239 Sequence
22	700.2	65.7	1119	4 AF266468	AF266468 Ovis arie
23	663.2	62.3	1440	10 MMU28406	MMU28406 Mus muscu
24	661.6	62.1	1080	10 AY049018	AY049018 Mus muscu
25	660	62.0	1185	10 MMU29677	MMU29677 Mus muscu
26	652	61.2	1315	10 RNRPCR3	RNRPCR3 Rattus norv
27	650.4	61.1	1080	6 AF003954	AF003954 Rattus no
28	637.8	59.9	7201	6 AX345238	AX345238 Sequence
29	636.2	59.7	1077	10 AF060698	AF060698 Cavia por
30	540.8	50.8	1495	9 HUMCCCKR1A	HUMCCCKR1A Homo sapi
31	540.8	50.8	1609	6 E13385	E13385 CDNA encod1
32	540.8	50.8	2156	6 HUMRANES	HUMRANES Homo sapien
33	540.8	50.8	2214	9 HUMHMI45	HUMHMI45 Human mRNa
34	540.8	50.8	197279	9 AC104439	AC104439 Homo sapi
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37	522	49.0	1056	4 AF127527	AF127527 Oryctolag
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41	480.8	45.1	1748	10 MMU28404	MMU28404 Mus muscu
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#### ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
AR164119	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
DEFINITION	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
ACCESSION	AR164119	Sequence	2 from patent US 6271347.	DNA	linear	PAT 17-OCT-2001
VERSION	AR164119.1	GI:16235065				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1065)					
AUTHORS	Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.					
TITLE	Eosinophil ectoxin receptor					
JOURNAL	Patent: US 6271347-A 2 07-AUG-2001.					
FEATURES	Location/Qualifiers					

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Best Local Similarity 100.0%; Pred. No. 7.1e-277;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCAACCTCAGTATGAGACCTTGGTACACATCTCTATGATGAGCTG 60
QY 61 GGCCTGCTGTGTAAGAGCTGATACAGAGCAGTATGAGCTGAGCTG 120
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Db 61 GGCCTGCTGTGTAAGAGCTGATACAGAGCAGTATGAGCTGAGCTG 120
QY 121 TACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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Db 121 TACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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Db 181 AAATACAGAGGCTCGCAATATGACCAACATCTGCTGCTGCTGCTG 240
QY 241 CTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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Db 301 TTGCGCATGAGCTGTAAGCTCTCTCAAGGTTTATACACAGAGCT 360
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QY 481 GCACTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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QY 541 ACTCTTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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Db 541 ACTCTTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CTGAGAAATGAGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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Db 661 GGAATCATCAAAAGGCTGAGAGTGGCCAGTAAAAAAGTCAAGG 720
QY 721 ATTCTTTCATCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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QY 901 TAGCCCTTGTGAGAGAGTTCGGAAGTACTGCGCACCTTCTTCA 960
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QY 1021 TCTGTCTCTCCATCCACAGAGAGCCGGAACCTCTATGCTGTT 1065
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Db 1021 TCTGTCTCTCCATCCACAGAGAGCCGGAACCTCTATGCTGTT 1065

RESULT 2
AX030929 1065 bp DNA linear PAT 20-SEP-2000
LOCUS Sequence 2 from Patent EP1012190.
DEFINITION AX030929
ACCESSION AX030929
VERSION AX030929.1 GI:10278334
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
TITLE Histophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 2 28-JUN-2000;
MERCK & CO INC (US)
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location/Qualifiers
source 1..1065
/organism="unidentified"
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BASE COUNT 230 a 289 c 242 g 304 t
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Query Match 100.0%; Score 1065; DB 6; Length 1065;
Best Local Similarity 100.0%; Pred. No. 7.1e-277;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAACCTCAGTATGAGACCTTGGTACACATCTCTATGATGAGCTG 60
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Db 1 ATGCAACCTCAGTATGAGACCTTGGTACACATCTCTATGATGAGCTG 60
QY 61 GGCCTGCTGTGTAAGAGCTGATACAGAGCAGTATGAGCTGAGCTG 120
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Db 61 GGCCTGCTGTGTAAGAGCTGATACAGAGCAGTATGAGCTGAGCTG 120
QY 121 TACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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Db 121 TACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 AAATACAGAGGCTCGCAATATGACCAACATCTACCTGCTCAAC 240
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Db 181 AAATACAGAGGCTCGCAATATGACCAACATCTACCTGCTCAAC 240
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Db 241 CTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TTGCGCATGAGCTGTAAGCTCTCTCAAGGTTTATACACAGAGCT 360
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Db 301 TTGCGCATGAGCTGTAAGCTCTCTCAAGGTTTATACACAGAGCT 360
QY 361 ATCTTTTCAATATCGCTGAGAAATGAGAGTATGCTGCTGCTG 420
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Db 361 ATCTTTTCAATATCGCTGAGAAATGAGAGTATGCTGCTGCTG 420
QY 421 GCCCTTGAGAGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Db 421 GCCCTTGAGAGCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GCACTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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Db 481 GCACTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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Db	601	CTGAGAAATGACCAATCTTCTGTCTCTCCCTCTGCTCTGCTATATGGCCATCTGCTACACA	660
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Qy	961	CTCAATGCACCTGGGGAGATATCATCCATTCCTCTAGTGTGAAGCTGGAAAGAACAGC	1020
Db	961	CTCAATGCACCTGGGGAGATATCATCCATTCCTCTAGTGTGAAGCTGGAAAGAACAGC	1020
Qy	1021	TCTGTCTCTCCATCCACAGCAGAGCGGGAACCTCTCTATTTGTGTTT	1065
Db	1021	TCTGTCTCTCCATCCACAGCAGAGCGGGAACCTCTCTATTTGTGTTT	1065
RESULT 3			
LOCUS	AF026535	1068 bp	linear PRI 02-NOV-1997
DEFINITION	Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.		
ACCESSION	AF026535		
VERSION	AF026535.1	GI:2582565	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1068) Xiao,L., Weiss,S., Qari,S., Rudolph,D., Hodge,T. and Lal,R. Partial resistance to infection by syncytium-inducing primary HIV-1 in exposed uninfected individuals homozygous for CCR3 32bp deletion		
AUTHORS	Unpublished		
JOURNAL	2 (bases 1 to 1068)		
REFERENCE	Qari,S.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (22-SEP-1997) Retrovirus Diseases Branch, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA		
FEATURES	Location/Qualifiers		
source	1..1068		
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Db 601	CTGAGAAATGACCATCTTCTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	100.0%	100.0%	1068
QY 661	GGAATCATTAACAAAGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAAGGCAATCCGGCTC	100.0%	100.0%	1068
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LOCUS Human eosinophil CC chemokine receptor 3 mRNA, complete cds.  
DEFINITION U28694  
ACCESSION U28694  
VERSION U28694.1 GI:1199579  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1200)  
AUTHORS Combadiere,C., Ahuja,S.K. and Murphy,P.M.  
TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor  
J. Biol. Chem. 270 (28), 16491-16494 (1995)  
JOURNAL MEDLINE 95348056  
PUBMED 7622448  
REFERENCE 2 (bases 1 to 1201)  
AUTHORS Combadiere,C.  
TITLE Direct Submission  
Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National Institutes of Health, Building 10, Room 11N11, Bethesda, MD 20892, USA

REFERENCE 3 (bases 1 to 1201)  
AUTHORS Combadiere,C., Ahuja,S.K. and Murphy,P.M.  
TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor  
J. Biol. Chem. 271 (18), 11034 (1996)  
JOURNAL MEDLINE 96210048  
PUBMED 8631926  
COMMENT On Feb 22, 1996 this sequence version replaced gi:881569.  
[Erratum J. Biol. Chem. 270 (1995) 30235].  
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CDS  
BASE COUNT 278 a 320 c 267 g 336 t  
ORIGIN

Query Match 100.0%; Score 1065; DB 9; Length 1201;  
Best Local Similarity 100.0%; Pred No. 7.2e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGACAACCTCAGTATGAGTGTGACCTTGTACACATCTACTATGATGACGTG 60  
Db 32 ATGACAACCTCAGTATGAGTGTGACCTTGTGACACATCTACTATGATGACGTG 91

Oy 61 GGCTGCTGTGTGAAGAGCTGATACAGACACTGATGGCCCGCGCTG 120  
Db 92 GGCTGCTGTGTGAAGAGCTGATACAGACACTGATGGCCCGCGCTG 120  
Oy 121 TACTCCCTGTGTGCTGCTGAGGCTGCTGAGGAGTGGTGTGATGATCTCATA 180  
Db 152 TACTCCCTGTGTGCTGCTGAGGCTGCTGAGGAGTGGTGTGATGATCTCATA 211  
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Db 212 AAATACAGAGAGCTCCCAATATGACCAATCTACTGCTCAACCTGGCCATTTGGAC 271  
Oy 241 CTGCTCTTCTGCTGACCTTCCATCTGATGATGATGATGAGGGGCTTAACTGGGTT 300  
Db 272 CTGCTCTTCTGCTGACCTTCCATCTGATGATGATGATGAGGGGCTTAACTGGGTT 331  
Oy 301 TTGGCCATGGCATGTGTAAGCTCCTCTGAGGCTTTATACACAGAGCTTGTACAGCAG 360  
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Oy 361 ATCTTTTCAATATCCCTGCTGACCAATGACAGTACTGGCCATTTGCTGCTGTTT 420  
Db 392 ATCTTTTCAATATCCCTGCTGACCAATGACAGTACTGGCCATTTGCTGCTGTTT 451  
Oy 421 GCCCTTGAGACCCGGAGCTGTCACCTTTGTGTCATCACAGCATGTCACCTGGGCTG 480  
Db 452 GCCCTTGAGACCCGGAGCTGTCACCTTTGTGTCATCACAGCATGTCACCTGGGCTG 511  
Oy 481 GCAGTGTACAGAGCTCTCTGTAATTTATCTTATGAGACTAAGAGTTGTTGAAGAG 540  
Db 512 GCAGTGTACAGAGCTCTCTGTAATTTATCTTATGAGACTAAGAGTTGTTGAAGAG 571  
Oy 541 ACCTTTGACAGTGTCTTTTCCAGAGAGATAGATATATGCTGGAGGCTTCCACACT 600  
Db 572 ACCTTTGACAGTGTCTTTTCCAGAGAGATAGATATATGCTGGAGGCTTCCACACT 631  
Oy 601 CTGAGATGACCATCTTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 632 CTGAGATGACCATCTTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691  
Oy 661 GGAATCATCAAAACGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 692 GGAATCATCAAAACGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751  
Oy 721 ATTTTGTGTCATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 752 ATTTTGTGTCATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811  
Oy 781 CTCTCTCTATCATCATCATCTTATTTGGAATGACTGTGAGGCGGAGCAAGCATCTGGAC 840  
Db 812 CTCTCTCTATCATCATCATCTTATTTGGAATGACTGTGAGGCGGAGCAAGCATCTGGAC 871  
Oy 841 CTGCTATGCTGTGACAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 872 CTGCTATGCTGTGACAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931  
Oy 901 TAGGCTTTGTTGGAAGAGCTTCCGGAAGTACTGCGGACCTTCTCCACAGGCACTTG 960  
Db 932 TAGGCTTTGTTGGAAGAGCTTCCGGAAGTACTGCGGACCTTCTCCACAGGCACTTG 991  
Oy 961 CTCATGACCTGGGACAGATCATCCATTCCTCTAGTGAGAGAGCTGGAAGAACACAGC 1020  
Db 992 CTCATGACCTGGGACAGATCATCCATTCCTCTAGTGAGAGAGCTGGAAGAACACAGC 1051  
Oy 1021 TCTGCTCTCCATCCACAGCAGACCGGAACCTCTATTTGTGTTT 1065  
Db 1052 TCTGCTCTCCATCCACAGCAGACCGGAACCTCTATTTGTGTTT 1096

RESULT 5  
AX334894 1717 bp DNA linear PAT 09-JAN-2002  
LOCUS AX334894  
DEFINITION Sequence 5403 from Patent WO0194629.

ACCESSION	AX334894	GI:18125613
VERSION	AX334894.1	
KEYWORDS		
SOURCE	human,	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horriigan,S., Soppel,D.R. and Weaver,Z.	
TITLE	Cancer gene determination and therapeutic screening using signature gene sets	
JOURNAL	Patent: WO 0194629-A 5403 13-DEC-2001; Avalon Pharmaceuticals (US)	
FEATURES	Location/Qualifiers	
SOURCE	1..1717	
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BASE COUNT	434 a 428 c 351 g 504 t	
ORIGIN		

Query Match	100.0%	Score 1065;	DB 6;	Length 1717;
Best Local Similarity	100.0%	Pred. No. 7.5e-277;		
Matches 1065; Conservative	0;	Mismatches	0;	Gaps 0

OY	1	ATGACAAACCTCACTGATACAGATTAGACCTTTGGTATACACATCCTACTATATACAGCG	60
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OY	61	GACCTGCTCTGTGAAAAAGCTGATACACAGACCACTGATAGGCCCACTTTTGGCCCCGTG	120
Dp	265	GACCTGCTCTGTGAAAAAGCTGATACACAGACCACTGATAGGCCCACTTTTGGCCCCGTG	324
OY	121	TACTCCCTGGAGTTTACATGCTGGGCCCTTTGGGCATATGAGTGGGTAGTATCCTCAATA	180
Dp	325	TACTCCCTGGAGTTTACATGCTGGGCCCTTTGGGCATATGAGTGGGTAGTATCCTCAATA	384
OY	181	AAATACAGAGAGGCTTCGAATTAATGACCAACATCTACCTGCTCAACCTGGCCATTTTGGAC	240
Dp	385	AAATACAGAGAGGCTTCGAATTAATGACCAACATCTACCTGCTCAACCTGGCCATTTTGGAC	444
OY	241	CTGCTCTTCCTGTCGACCCCTTCATCTCGAGATCCACTATGTCAGGGGGCCATTAACGCGGT	300
Dp	445	CTGCTCTTCCTGTCGACCCCTTCATCTCGAGATCCACTATGTCAGGGGGCCATTAACGCGGT	504
OY	301	TTTGGCCATGGCAGTGTAAAGCTCCTCTCAGGGTTTATACACAGCGCTTGATACAGCAG	360
Dp	505	TTTGGCCATGGCAGTGTAAAGCTCCTCTCAGGGTTTATACACAGCGCTTGATACAGCAG	564
OY	361	ATCTTTTTCATATATCTCTGCTGACAAATCGACAGATACCTGGCCATTTGCCATGCTGTGTT	420
Dp	565	ATCTTTTTCATATATCTCTGCTGACAAATCGACAGATACCTGGCCATTTGCCATGCTGTGTT	624
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Dp	625	GCCCTTCGAGCCCGGAGCTGTCATCTTTGGTGCATACACAGCATGTCACCGGGGGCCG	684
OY	481	GCAGTGTACGACGCTTCTCTGTAATTTATCTTCTATGAGACTGAAGAGTGTGTTGAAGAG	540
Dp	685	GCAGTGTACGACGCTTCTCTGTAATTTATCTTCTATGAGACTGAAGAGTGTGTTGAAGAG	744
OY	541	ACTCTTTGACAGGCTTTTACCCAGAGATACAGTATATAGCTGAGAGCATTTCCACACT	600
Dp	745	ACTCTTTGACAGGCTTTTACCCAGAGATACAGTATATAGCTGAGAGCATTTTCCACACT	804
OY	601	CTGAGAAATGACCATTCTTGTCTCCCTTCCTGCTGCTGTTATGGCCATCTGTATACAA	660
Dp	805	CTGAGAAATGACCATTCTTGTCTCCCTTCCTGCTGCTGTTATGGCCATCTGTATACAA	864
OY	661	GGAATCATCAAAACCGCTGTGAGTGGCCCCAGTAAAAAAAAGTACAGGCCATCCGGCTC	720
Dp	865	GGAATCATCAAAACCGCTGTGAGTGGCCCCAGTAAAAAAAAGTACAGGCCATCCGGCTC	924

OY	721	ATTTTGTGCATCAGCGCGTGTTTTTCATTTTTCGAGACCCCTCAATGTGGTATCTTT	780
Db	925	ATTTTGTGCATCAGCGCGTGTTTTTCATTTTTCGAGACCCCTCAATGTGGTATCTTT	984
OY	781	CTCTCTTCTCATTCATCCATCTTATTTTGGAAATGACTGTAGCGGAGCAGCATCTGGAC	840
Db	985	CTCTCTTCTCTATTCATATCCATCTTATTTTGGAAATGACTGTAGCGGAGCAGCATCTGGAC	1044
OY	841	CTGGTCATGCGAGGTGACAGAGGTGATGCTGCCTACTCCACTCTGCATGACCCGGTGATC	900
Db	1045	CTGGTCATGCGAGGTGACAGAGGTGATGCTGCCTACTCCACTCTGCATGATACCCGGTGATC	1104
OY	901	TACGCCCTTTGTTGGAGAGGTTCCGGAAGTACTGCGCCACTTCTTCACAGGCACCTTG	960
Db	1105	TACGCCCTTTGTTGGAGAGGTTCCGGAAGTACTGCGCCACTTCTTCACAGGCACCTTG	1164
OY	961	CTCATGCACTGGGCGAGATACATCCCATTCCTCCTTAGTGAAGACTGGAAAGAACAGC	1020
Db	1165	CTCATGCACTGGGCGAGATACATCCCATTCCTCCTTAGTGAAGACTGGAAAGAACAGC	1224
OY	1021	TCTGTCTCTCCATCCACAGCAGAGCGGCACTCTCTATGTGTGTTT	1065
Db	1225	TCTGTCTCTCCATCCACAGCAGAGCGGCACTCTCTATGTGTGTTT	1269

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
HSU51241	Human eosinophil ectaxin receptor (CMKMR3) gene, complete cds.	U51241	U51241.1	GI:1480480	1717 bp	DNA	Linear	PRI 09-OCT-1996				
HSU51241						homo sapiens.						
						Homo sapiens.						
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
						Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
						1 (bases 1 to 1717)						
						Daugherty, B.L., Siciliano, S.J., Demartino, J.A., Malkowitz, L.,						
						Sitolina, A. and Springer, M.S.						
						Cloning, expression, and characterization of the human eosinophil						
						ectaxin receptor						
						J. Exp. Med. 183 (5), 2349-2354 (1996)						
						9623504						
						8642344						
						2 (bases 1 to 1717)						
						Daugherty, B.L.						
						Direct Submission						
						Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,						
						Merck Research Laboratories, RDW-107, P.O. Box 2000, Rahway, NJ						
						07065, USA						

FEATURES	SOURCE	LOCATION/Qualifiers
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		/protein_id="AAB16831.1"
		/db_xref="GI:1480481"
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Query Match 100.0%; Score 1065; DB 9; Length 1717;  
Best Local Similarity 100.0%; Pred. No. 7.5e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAACCTCAGTATGACAGCTTGGTACACATCTCTATGATGACGTG 60  
DB 205 ATGCAACCTCAGTATGACAGCTTGGTACACATCTCTATGATGACGTG 264  
QY 61 GGCGTCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCAGTTGTGCCCGCTG 120  
DB 265 GGCGTCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCAGTTGTGCCCGCTG 324  
QY 121 TACTCCCTGGTTCACCTGTGGGCTCTTGGGCAATGTGTGTGTGATGATCCTCATA 180  
DB 325 TACTCCCTGGTTCACCTGTGGGCTCTTGGGCAATGTGTGTGTGATGATCCTCATA 384  
QY 181 AAATACAGAGGCTCCGAAATATGACCAACATCACTGCTCAACCTGGCCATTTCGGAC 240  
DB 385 AAATACAGAGGCTCCGAAATATGACCAACATCACTGCTCAACCTGGCCATTTCGGAC 444  
QY 241 CTGCTCTCTCTCTCACCCTTCATTCGATCCATATGTCAGGGGGCATTAACCTGGGT 300  
DB 445 CTGCTCTCTCTCTCACCCTTCATTCGATCCATATGTCAGGGGGCATTAACCTGGGT 504  
QY 301 TTGGCCATGGCATGTGTAGCTCCTCTCAGGGTTTATACACAGGCTTGTACAGGAG 360  
DB 505 TTGGCCATGGCATGTGTAGCTCCTCTCAGGGTTTATACACAGGCTTGTACAGGAG 564  
QY 361 ATCTTTTCAATATCGCTGCTGCTGACATGACAGGTACCTGGCCATTGCTCAGCTGTTT 420  
DB 565 ATCTTTTCAATATCGCTGCTGCTGACATGACAGGTACCTGGCCATTGCTCAGCTGTTT 624  
QY 421 GCCCTTGAGGCCGAGCTGTCATTTGTGTGTCATCACAGACATGTCACCTGGGGCTG 480  
DB 625 GCCCTTGAGGCCGAGCTGTCATTTGTGTGTCATCACAGACATGTCACCTGGGGCTG 684  
QY 481 GCACTGCTAGAGCTCTTCCGAAATTTATCTTATGAGACTGAAGCTGTGGAAGAG 540  
DB 685 GCACTGCTAGAGCTCTTCCGAAATTTATCTTATGAGACTGAAGCTGTGGAAGAG 744  
QY 541 ACTGTTGACAGTCTCTTTTACCAGAGATACATATATAGCTGAGGCAATTTCCACACT 600  
DB 745 ACTGTTGACAGTCTCTTTTACCAGAGATACATATATAGCTGAGGCAATTTCCACACT 804  
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DB 805 CTGGAATGACATCTTCTGTCTCTGCTCCCTGCTGCTGCTGCTTATGGCCATCTGCTACACA 864  
QY 661 GGAATCATCAAAAGCGCTGAGGTGCCCCAGTAAAAAAAGTCAAGGCCATCCGCTC 720  
DB 865 GGAATCATCAAAAGCGCTGAGGTGCCCCAGTAAAAAAAGTCAAGGCCATCCGCTC 924  
QY 721 ATTGTTGTCATCAGGCGGTGTTTTCATTTTTCGACACCCCTCAATGTTGGTATGCTT 780  
DB 925 ATTGTTGTCATCAGGCGGTGTTTTCATTTTTCGACACCCCTCAATGTTGGTATGCTT 984  
QY 781 CTCTCTCTCATCAATCATCTTATTTGGAATAGCTGTAGCGGAGCAAGCATCTGGAC 840  
DB 985 CTCTCTCTCATCAATCATCTTATTTGGAATAGCTGTAGCGGAGCAAGCATCTGGAC 1044  
QY 841 CTGCTCATGCTGGTGACAGAGGTATCGCTACTCCACAGCTGCTGCATGAACCCGGTATC 900  
DB 1045 CTGCTCATGCTGGTGACAGAGGTATCGCTACTCCACAGCTGCTGCATGAACCCGGTATC 1104  
QY 901 TACGCTTTGTTGGAGAGAGTTCCGGAAGTACTGGGCACTCTTCCACAGGCACTTGG 960  
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QY 961 CTGATGACCTGGGCAATACATCCATCTCTCTAGTGAAGAGCTGGAAGAACAGC 1020  
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QY 1021 TCTGTCTCTCATATCCACAGAGCGGAACTCTCTATTTGTTT 1065

DB 1225 TCTGTCTCTCATATCCACAGAGCGGCAACTCTCTATGTGTTT 1269

RESULT 7  
BD006761 1915 bp DNA linear PAR 31-JAN-2002  
LOCUS  
DEFINITION  
Chemokine receptors 88-2b [CCR-3] and 88c and antibodies thereof.  
ACCESSION  
BD006761  
VERSION  
BD006761.1 GI:18635132  
KEYWORDS  
JP 2001029089-A/2.  
SOURCE  
unidentified.  
ORGANISM  
unclassified.  
REFERENCE  
1 (bases 1 to 1915)  
AUTHORS  
Gary P.W., Sheicart, V.L. and Rayport, C.J.  
TITLE  
Chemokine receptors 88-2b [CCR-3] and 88c and antibodies thereof  
JOURNAL  
Patent: JP 2001029089-A 2 06-FEB-2001;  
ICOS CORP  
COMMENT  
OS Unidentified  
PN JP 2001029089-A/2  
PD 06-FEB-2001  
PE 16-MAY-2000 JP 2000143832  
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI  
PATRICK W GARY, VICMIL L, SHEICART, CARROLL J RAYPORT PC  
C12N15/09, C07K14/715, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12P1/68, G01N33/15, PC  
G01N33/50,  
PC G01N33/53, G01N33/566//A61K39/395, A61K39/395, A61K45/00,  
A61P7/02, PC A61P17/06,  
PC A61P19/02, A61P29/00, A61P31/12, (C12P21/02, C12R1:91), C12N15/00,  
PC C12N5/00,  
PC C12N5/00, C12N15/00  
CC Strandedness: Single:  
CC Topology: Linear:  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
1..1915  
location/Qualifiers  
BASE COUNT 488 a 470 c 373 g 584 t  
ORIGIN

Query Match 100.0%; Score 1065; DB 5; Length 1915;  
Best Local Similarity 100.0%; Pred. No. 7.6e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAACCTCAGTATGACAGCTTGGTACACATCTCTATGATGACGTG 60  
DB 362 ATGCAACCTCAGTATGACAGCTTGGTACACATCTCTATGATGACGTG 421  
QY 61 GGCGTCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCAGTTGTGCCCGCTG 120  
DB 422 GGCGTCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCAGTTGTGCCCGCTG 481  
QY 121 TACTCCCTGGTTCACCTGTGGGCTCTTGGGCAATGTGTGTGTGATGATCCTCATA 180  
DB 482 TACTCCCTGGTTCACCTGTGGGCTCTTGGGCAATGTGTGTGTGATGATCCTCATA 541  
QY 181 AAATACAGAGGCTCCGAAATATGACCAACATCACTGCTCAACCTGGCCATTTCGGAC 240  
DB 542 AAATACAGAGGCTCCGAAATATGACCAACATCACTGCTCAACCTGGCCATTTCGGAC 601  
QY 241 CTGCTCTCTCTCTCACCCTTCATTCGATCCATATGTCAGGGGGCATTAACCTGGGT 300  
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QY 301 TTGGCCATGGCATGTGTAGCTCCTCTCAGGGTTTATACACAGGCTTGTACAGGAG 360  
DB 662 TTGGCCATGGCATGTGTAGCTCCTCTCAGGGTTTATACACAGGCTTGTACAGGAG 721

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1021 TCGTCTTCCATCCACAGAGAGCGGGAAGTCTATTTGTTT 1065  
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1382 TCGTCTTCCATCCACAGAGAGCGGGAAGTCTATTTGTTT 1426  
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RESULT 8  
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LOCUS AF247361  
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.  
ACCESSION AF247361 GI:19110542  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 5791)  
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
Michael,N.L.  
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
for a Rare TATA-less Promoter Structure Conserved between  
Drosophila and Humans  
JOURNAL MEDLINE  
22074933  
Genomics 80 (1), 86-95 (2002)  
PUBMED 12079287  
2 (bases 1 to 5791)  
Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
REFERENCE AUTHORS Direct Submission  
TITLE JOURNAL  
Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.

FEATURES  
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Best Local Similarity 100.0%; Pred. No. 8.6e-277;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ATGACAACTCACTAGATACAGTTGAGACCTTGGTACCAATCTTACATGATGACGTG 60  
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Db	4375	ATCTTTTTCATAATTCCTGCTGACAAATGCAAGTACCTACGGCATCTGTCCATAGCTGTGTTT	4434
QY	421	GCCCTTCGAGCCCGGAGCTGTACATTTTGGTGTCAATCACAGCATGTCACCTGGGGCTG	480
Db	4435	GCCCTTCGAGCCCGGAGCTGTACATTTTGGTGTCAATCACAGCATGTCACCTGGGGCTG	4494
QY	481	GCAGGCGTAGAGAGCTTCCTGGAATTTATCTTATGTGAGCTGAAGAGTTGTTTAAGAG	540
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QY	541	ACTCTTTGACAGTGCCTTTTACCAGAGAGATACAGATATAGCTGGAGGCAATTTCCAACT	600
Db	4555	ACTCTTTGACAGTGCCTTTTACCAGAGAGATACAGATATAGCTGGAGGCAATTTCCAACT	4614
QY	601	CTGAGATGACCATCTTCTGTCTGTCTTCCCTCTGCTGCTTTAGGCGCATCTGTACACA	660
Db	4615	CTGAGAAAGACCATCTTCTGTCTGTCTTCCCTCTGCTGCTTTAGGCGCATCTGTACACA	4674
QY	661	GGAAATCATCAAAAGCGCTCTGAGGGGCCCGAGTAAAAAAAGTACAAGGCATCCGGCTC	720
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Db	4735	ATTTTGTGCATCANGGCGGTGTTTTTCATTTTCTGACACCCATACATGTGGCTATCTTT	4794
QY	781	CTCTCTCCATCAATCAATCCATCTTATTTTGGAAATGACTGTGAGCGGAGCATCTGGAC	840
Db	4795	CTCTCTCCATCAATCAATCCATCTTATTTTGGAAATGACTGTGAGCGGAGCATCTGGAC	4854
QY	841	CTGGTCATGCTGTGTGACAGAGGTATATGCCCTTACTCTCCACTGTGATTAACCCGGTGATC	900
Db	4855	CTGGTCATGCTGTGTGACAGAGGTATATGCCCTTACTCTCCACTGTGATTAACCCGGTGATC	4914
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Db	4915	TACGCGCTTTGGTGGAGAGAGTTCGGAAAGTACCTGGCGCACTTTTCCACAGGAGCATTG	4974
QY	961	CTCATGCACCTGTGGCGAGATATCCCATTTCTCTCTAGTGAAGACCTGGAAAGAACACAGC	1020
Db	4975	CTCATGCACCTGTGGCGAGATATCCCATTTCTCTCTAGTGAAGACCTGGAAAGAACACAGC	5034
QY	1021	TCTGTCTCTCCATCTCACAGCAGAGCCGGAACCTCTTATTTGTGTTT	1065
Db	5035	TCTGTCTCTCCATCTCACAGCAGAGCCGGAACCTCTTATTTGTGTTT	5079
RESULT 9			
LOCUS	AC104439	197279 bp	DNA linear PRI 20-JUN-2002
DEFINITION	Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.		
ACCESSION	AC104439	AC024739	
VERSION	AC104439.2	GI:21490240	
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenplimachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.		
TITLE	Direct Submission		
REFERENCE	2 (bases 1 to 197279)		
AUTHORS	Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
REFERENCE	3 (bases 1 to 197279)		
AUTHORS	Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenplimachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.		

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TITLE      Direct Submission
JOURNAL    Submitted (20-JUN-2002) Genome Center, University of Washington,
           Box 352145, Seattle, WA 98195, USA
COMMENT    On Jun 20, 2002 this sequence version replaced gi.17488621.

Center: University of Washington Genome Center
Center Code: UMGCC
Web Site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: WUGSC

----- Project Information -----
Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)

----- Summary Statistics -----
Sequencing vector: unknown: 52% of reads
Sequencing vector: plasmid: L08752: 48% of reads
Chemistry: Dye-terminator ET: 94% of reads
Chemistry: Dye-terminator Big Dye: 6% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

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Overlapping Sequences:
5' : RP11-91E8 (UMGC:bc0216) AC026349
3' : CTD-2563A18 (UMGC:bc0730)

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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

-----
Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

HindIII      BglII      EcoRI

SeqDerMap  FngRPrnt  SeqDerMap  FngRPrnt  SeqDerMap  FngRPrnt
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2687      2617      8949      8586      8696      8661
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6382      6410      2067      2160      6      <800
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512      <800      7846      7940      2742      2803
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449      <800      3734      3895      5376      5324
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2602      2763      1334      1301      1493      1478

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1711	1683	691	<800	2900	2954
9821	9472	5477	5348	1484	1478
516	<800	305	<800	1005	995
8587	8291	25245	25541	1181	1171
7446	7581	3988	4121	18560	19002
2088	2075	1633	1598	3603	3579
2509	2617	631	<800	4943	5076
3519	3501	90	<800	3239	3241
26	<800	402	<800	953	995
925	933	3350	3490	1621	1615
98	<800	4577	4515	6827	6900
6409	6410	1229	1183	79	<800
1383	1376	4221	4331	16418	16263
16048	15829	3980	4121	3361	3241
1876	1877	2548	2497	872	881
4169	4068	674	<800	4220	4193
1674	1683	2332	2309	2848	2803
52	<800	11445	11045	2283	2318
5227	5082	5692	5632	3211	3241
15464	15829	1385	1414	4615	4632
14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3266	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2758	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800

1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
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862	854	2500	2497	4731	4632
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Query Match 100.0%; Score 1065; DB 9; Length 197279;  
Best Local Similarity 100.0%; Pred. No. 1.3e-276;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1	ATGACAACTCTAGATACAGTGTGAGACCTTTGGTACACATCTACTATGATGACGTG	60
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QY 61	GGCCTCTCTGTAAAAAGTGTATACAGAGCATATGGCCCAAGTTTGGCCCGCTG	120
DB 190248	GGCCTCTCTGTAAAAAGTGTATACAGAGCATATGGCCCAAGTTTGGCCCGCTG	190307
QY 121	TACTCCCTGTTCACCTGTGGGCTCTTGGCAATGTGGTGTGATGATCTCATATA	180
DB 190308	TACTCCCTGTTCACCTGTGGGCTCTTGGCAATGTGGTGTGATGATCTCATATA	190367
QY 181	AAATACAGAGGCTCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGAC	240
DB 190368	AAATACAGAGGCTCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTGCGAC	190427
QY 241	CTGCTCTCTCTGTCACCTTCATCTGTGATCCATATGTACGGGGGCTTAACCTGGTT	300
DB 190428	CTGCTCTCTCTGTCACCTTCATCTGTGATCCATATGTGATCCATATGTGATCCATAT	190487
QY 301	TTTGGCCATGGCATGTGTAACTCTCTCAGGGTTTATACACAGAGCTTGTACAGCGAG	360
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QY 361	ATCTTTTTCATTAATCTGCTGACAAATCGACAGGTACCTGGCCATTTGCAATGCTGTGTTT	420
DB 190548	ATCTTTTTCATTAATCTGCTGACAAATCGACAGGTACCTGGCCATTTGCAATGCTGTGTTT	190607
QY 421	GGCCTTCGAGCCCGGACGTGCTACTTTTGGTGTATACACAGCATCTGACCTGGGGCTTG	480
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QY 481	GCAGTGTACAGCTCTTCTGTAATTTATCTTATGAGACTGAAGAGTTGTTGAAGAG	540
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FEATURES  
\* 218210 219800: contig of 1591 bp in length  
\* 219801 219900: gap of 100 bp  
\* 219901 220965: contig of 1065 bp in length.  
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/chromosome="3"  
/map="3p21.3"  
/clone="RP6-32g23"  
BASE COUNT 62577 a 44674 c 45661 g 65453 t 2600 others  
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Best Local Similarity 100.0%; Pred. No. 1.3e-276;  
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 GGCTGCTGTGTAAGAGGTGATACAGAGCATGATGCGCCAGTTTGCCCGCTG 120  
DB 140324 GGCTGCTGTGTAAGAGGTGATACAGAGCATGATGCGCCAGTTTGCCCGCTG 140383  
QY 121 TACTCCCTGCTGTTCACTGTGGCTCTTGGGCAATGTGGTGGTATGATCTCAT 180  
DB 140384 TACTCCCTGCTGTTCACTGTGGCTCTTGGGCAATGTGGTGGTATGATCTCAT 140443  
QY 181 AATATACAGAGGCTCCGAATATGACCAACATCTACCTGCTCAACCTGCCATTTGCGAC 240  
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DB 140624 ATCTTTTCAATAATCTCTGCTGACATCGACAGAGTACCTGGCCATTTGCCATGCTGTT 140683  
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QY 481 GCAGCTGACAGAGCTCTTCTGTAATTTATCTTATGAGAGTGAAGAGTGTGAAGAG 540  
DB 140744 GCAGCTGACAGAGCTCTTCTGTAATTTATCTTATGAGAGTGAAGAGTGTGAAGAG 140803  
QY 541 ACTCTTTGCAAGTCTTTTACCAAGAGATACAGTATATAGCTGAGAGCACTTTCCACACT 600  
DB 140804 ACTCTTTGCAAGTCTTTTACCAAGAGATACAGTATATAGCTGAGAGCACTTTCCACACT 140863  
QY 601 CTGAGATGACCATCTTCTGTCTGTTCTCCCTGCTGCTGTTATGAGCAATCTCTACACA 660  
DB 140864 CTGAGATGACCATCTTCTGTCTGTTCTCCCTGCTGCTGTTATGAGCAATCTCTACACA 140923  
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LOCUS AX280851  
DEFINITION Sequence 474 from Patent WO0177172.  
ACCESSION AX280851  
VERSION AX280851.1 GI:16608181  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.  
Non-endogenous, constitutively activated known g protein-coupled  
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Patent: WO 0177172-A 474 18-OCT-2001;  
Arena Pharmaceuticals, Inc. (US)  
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Query Match 99.7%; Score 1061.8; DB 6; Length 1068;  
Best Local Similarity 99.8%; Pred. No. 5.2e-276;  
Matches 1063; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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RESULT 12  
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DEFINITION Sequence 2 from Patent WO0192520.  
AX323054  
VERSION AX323054.1 GI:18093940  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Barnes, A.A., Fraser, N.J., O'Shaughnessy, C.T. and Wise, A.G.  
TITLE Modified chemokine receptor ccr-3 and assay  
JOURNAL Patent: WO 0192520-A 2 06-DEC-2001;  
GIAOX GROUP LIMITED (GB)  
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BASE COUNT 231 a 289 c 243 g 305 t  
ORIGIN  
Query Match 99.7%; Score 1061.8; DB 6; Length 1068;  
Best Local Similarity 99.8%; Pred. No. 5.2e-276;  
Matches 1063; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DEFINITION	Human C-C chemokine receptor 3 (CCR-3) gene, complete cds.				
ACCESSION	U49727				
VERSION	U49727.1	GI:1477560			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 1689)				
JOURNAL	Ponath,P.D., Qin,S., Post,T.W., Wang,J., Wu,L., Gerard,N.P.,				
MEDLINE	Newman,W., Gerard,C. and Mackay,C.R.				
PUBMED	Molecular cloning and characterization of a human eotaxin receptor				
REFERENCE	J. Exp. Med. 183 (6), 2437-2448 (1996)				
AUTHORS	96281895				
TITLE	8676064				
JOURNAL	2 (bases 1 to 1689)				
MEDLINE	Ponath,P.D.				
PUBMED	Direct Submission				
REFERENCE	Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,				
AUTHORS	Leukosite, Inc., 215 First St., Cambridge, MA 02118, USA				
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DEFINITION	Homo sapiens gene for b-chemokine receptor CCR3, complete cds.	linear	PRI 25-NOV-1999
ACCESSION	AB023887		
VERSION	AB023887.1	GI:5467132	
KEYWORDS	b-chemokine receptor CCR3.		
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